

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:20:15 ; Search time 76.45 Seconds

(without alignments)  
176,502 Million cell updates/sec

Title: US-09-351-778a-9

Sequence: 1 MTCSTIAPTDTYRNTATNGL.....ICCLKRRAAPRIPIIVL 78

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 562222 segs, 172994929 residues

Word size: 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

SPRMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	92.3	101	12	091023 human adeno
2	56	71.8	101	12	091236 human adeno
3	18	23.1	94	12	012392 human adeno
4	7	9.0	83	12	088422 human adeno
5	7	9.0	87	10	084862 spiroplasma
6	7	9.0	160	16	098268 oryza sativ
7	7	9.0	160	16	092XL7 rhizobium 1
8	7	9.0	197	16	09JSG7 rhizobium m
9	7	9.0	228	2	09JSG7 chlamydia p
10	7	9.0	245	8	09RHX8 pseudomonas
11	7	9.0	316	10	09C9X6 nephroblast
12	7	9.0	387	16	099X15 arabidopsis
13	7	9.0	391	16	087GC3 staphylococ
14	7	9.0	392	10	08AX94 clostridium
15	7	9.0	490	10	09AX94 oryza sativ
16	7	9.0	536	5	09FSS8 oryza sativ
					045994 caenorhabd1

17	7	9.0	604	5	09VQ31 drosophila
18	7	9.0	635	5	09VJ77 drosophila
19	7	9.0	649	5	09NKD0 drosophila
20	7	9.0	965	2	032494 bacteroides
21	7	9.0	1175	16	091356 pseudomonas
22	7	9.0	2689	5	095Y78 leishmania
23	6	7.7	26	4	09BUB3 homo sapien
24	6	7.7	53	13	09YH36 homo sapien
25	6	7.7	64	2	09E347 streptomyces
26	6	7.7	69	13	09DEC6 gallus gall
27	6	7.7	73	15	087603 chimpanzee
28	6	7.7	76	4	096EN4 homo sapien
29	6	7.7	77	12	064888 avian adeno
30	6	7.7	89	10	094J51 oryza sativ
31	6	7.7	89	16	09AAB7 candida
32	6	7.7	91	4	09H4V4 homo sapien
33	6	7.7	94	16	09PCB2 xylella fas
34	6	7.7	94	16	09PCAS xylella fas
35	6	7.7	95	11	090ZG8 rictus norv
36	6	7.7	97	3	09Y7L9 schistosom
37	6	7.7	113	16	09K1B1 neisseria m
38	6	7.7	113	16	09JX91 streptomyces
39	6	7.7	115	2	09KXU2 ashya goss
40	6	7.7	115	3	09P8V1 pseudomonas
41	6	7.7	119	16	09HAX8 frankia sp.
42	6	7.7	126	2	09Z5Y0 rhizobium m
43	6	7.7	126	16	092VV9 vibrio para
44	6	7.7	128	2	094950 sulfolobus
45	6	7.7	129	12	0914M0

## ALIGNMENTS

RESULT 1

091023 PRELIMINARY; PRT: 101 AA.

AC 091023: 01-DEC-2001 (TREMREL. 19, Created)

DT 01-DEC-2001 (TREMREL. 19, Last sequence update)

DT 01-DEC-2001 (TREMREL. 19, Last annotation update)

DE 11.6K PROTEIN.

OS Human adenovirus type 2.

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI\_TaxID=10515;

RN (1)

RP SEQUENCE FROM N.A.

RA Borchering F., Pring-Akerblom P.

RT "Adenoviruses of subgenus c with different organ tropism."

RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ293915; CAC67721.1; "

SO SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;

Query Match 92.3%; Score 72; DB 12; Length 101;

Best Local Similarity 100.0%; Pred. No. 3.4e-70;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 APTDYYRNTATGTSALNPQVHAFVNDMASLDMWFSIALMFVCLLIIMLLICCKRRR 66

DB 7 APTDYYRNTATGTSALNPQVHAFVNDMASLDMWFSIALMFVCLLIIMLLICCKRRR 66

OY 67 ARPIYPIPIIVL 78

DB 67 ARPIYPIPIIVL 78

RESULT 2

OY 091236 PRELIMINARY; PRT: 101 AA.

AC 091236: 01-DEC-2001 (TREMREL. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE 11.6K PROTEIN.  
 OS Human adenovirus type 2.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=10515;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PREI:  
 RA Borchering F., Pring-Akerblom P.;  
 RT "Adenoviruses of subgenus C with different organ tropism";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ293913; CAC6704.1; -  
 SO SEQUENCE 101 AA; 11704 MW; E13857DC5891E85B CRC64;

Query Match 71.8%; Score 56; DB 12; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-53;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ALNLPQVNAFVNDASLDMMFSLAMFVCLIMLCLCKRRRRPRPIPIVL 78  
 DB 23 ALNLPQVNAFVNDASLDMMFSLAMFVCLIMLCLCKRRRRPRPIPIVL 78

RESULT 3  
 ID 012392 PRELIMINARY; PRT; 94 AA.  
 AC 012392;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last annotation update)  
 DE 11.6K PROTEIN.  
 GE AD1/E3-11.6K.  
 OS Human adenovirus type 1.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=10533;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-HANNOVER / ADRIAN;  
 RA Reichmann H., Scharschmidt E., Geisler B., Hausmann J., Ortman D.,  
 RA Bauer U., Flunker G., Seidel W.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y11257; CAA72127.1; -  
 SO SEQUENCE 94 AA; 10674 MW; D1148B5AF771862 CRC64;

Query Match 23.1%; Score 18; DB 12; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 MMFSLAMFVCLIML 58  
 DB 35 MMFSLAMFVCLIML 52

RESULT 4  
 ID 088422 PRELIMINARY; PRT; 83 AA.  
 AC 088422;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE SPV1-C74, COMPLETE GENOME.  
 OS Spiloplasma virus.  
 OC Viruses; unclassified viruses.  
 OX NCBI\_TaxID=12338;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPV1-C74;  
 RA Beddar C.M., Aulio P., Bove J., Renaudin J.;  
 RT "Spiloplasma citri virus SPV1. Characterization of viral sequences

RT present in the spiroplasma host chromosome.";  
 RL Curr. Microbiol. 32:1-7(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPV1-C74;  
 RA Renaudin J.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U28974; AAA85015.1; -  
 SO SEQUENCE 83 AA; 9398 MW; DA969373B02BFFA8 CRC64;

Query Match 9.0%; Score 7; DB 12; Length 83;  
 Best Local Similarity 100.0%; Pred. No. 7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSL 24  
 DB 30 TGLTSL 36

RESULT 5  
 ID 09462 PRELIMINARY; PRT; 87 AA.  
 AC 09462;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE HYPOTHETICAL 9.9 KDA PROTEIN.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriarthroideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. NIPPONBARE;  
 RA Beil C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,  
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsirlin T.,  
 RA Riggs F., Hsiao J., Zismann V., Blunt S., Pal G., VanAken S.E.,  
 RA Uteback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,  
 RA White O., Fraser C.M.;  
 RT "Oryza sativa chromosome 3 BAC OSJNB0057P11 genomic sequence.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC084767; AAK72273.1; -  
 KW Hypothetical protein.  
 SO SEQUENCE 87 AA; 9941 MW; 092E2A6E9D0A42CE CRC64;

Query Match 9.0%; Score 7; DB 10; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 7.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LKRRAR 68  
 DB 48 LKRRAR 54

RESULT 6  
 ID 098268 PRELIMINARY; PRT; 160 AA.  
 AC 098268;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE MUR9079 PROTEIN.  
 GE MUR9079.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-MAFE30309;  
 MEDLINE-21082930; PubMed-11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,  
 RA Takuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL: AP003015; BAB54491.1; -  
 KW Plasmid; Complete proteome.  
 SQ SEQUENCE 160 AA; 17696 MW; 85A9C5A9233D9A50 CRC64;

Query Match  
 Best Local Similarity 9.0%; Score 7; DB 16; Length 160;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSITAP 8  
 DB 28 TGSITAP 34

RESULT 7  
 ID 092XL7 PRELIMINARY; PRT; 160 AA.  
 AC 092XL7;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE HYPOTHETICAL PROTEIN SMA2279.  
 GN SMA2279.  
 OS Rhizobium melioli (Sinorhizobium melioli).  
 OC plasmid pSymb (megaplasmid 1).  
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_Taxid:382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-1021;  
 RX MEDLINE-21396509; PubMed-11481432;  
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,  
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,  
 RA Curjel M., Hong A., Huizer L., Hyman R.W., Kahn D., Kahn M.L.,  
 RA Kallman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,  
 RA Yen K.-C., Davis R.W., Federspiel N.A., Long S.R.;  
 RT "Nucleotide sequence and predicted functions of the entire  
 RT Sinorhizobium melioli pSymb megaplasmid";  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9883-9886(2001).  
 DR EMBL: AE007307; AAK65885.1; -  
 KW Hypothetical protein; Plasmid; Complete proteome.  
 SQ SEQUENCE 160 AA; 17966 MW; 98B4EBE18A1BE34 CRC64;

Query Match  
 Best Local Similarity 9.0%; Score 7; DB 16; Length 160;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSITAP 8  
 DB 28 TGSITAP 34

RESULT 8  
 ID 09JSG7 PRELIMINARY; PRT; 197 AA.  
 AC 09JSG7;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE C1142 HYPOTHETICAL PROTEIN\_2.  
 GN CP00259.

OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
 OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales.  
 OX NCBI\_Taxid:83558;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-J138;  
 RX MEDLINE-20330349; PubMed-10871362;  
 RA Shihai M., Hlirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
 RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;  
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
 RT from Japan and CML029 from USA";  
 RL Nucleic Acids Res. 28:2311-2314(2000).  
 DR EMBL: AP002545; BAA98469.1; -  
 DR InterPro: IPR001899; Gram\_pos\_anchor.  
 DR InterPro: IPR000531; TonB\_dox.  
 DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
 DR PROSITE: PS00430; TONB\_DEPENDENT\_REC\_1; UNKNOWN\_1.  
 SQ SEQUENCE 197 AA; 22016 MW; EAA69A27851F790D CRC64;

Query Match  
 Best Local Similarity 9.0%; Score 7; DB 16; Length 197;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23  
 DB 74 ATGLTSA 80

RESULT 9  
 ID 09RBX8 PRELIMINARY; PRT; 228 AA.  
 AC 09RBX8;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE HYPOTHETICAL 24.1 KDA PROTEIN.  
 OS Pseudomonas indologfera.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Vogesella.  
 OX NCBI\_Taxid:45465;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC19706;  
 RA van de Lo F.J., Keese P., Llewellyn D.;  
 RT "Structural and regulatory genes controlling indigoidine production in  
 RT Vogesella indologfera: Involvement of a peptide synthetase homolog";  
 RL Submitted (SPP-1998) to the EMBL/Genbank/DBJ databases.  
 CC -I- SIMILARITY: BELONGS TO THE TETR/ACR FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.  
 DR EMBL: AF088856; AAD54003.1; -  
 DR InterPro: IPR001647; HTH\_Tetr.  
 DR Pfam: PF00440; tetr\_1.  
 DR PRINTS: PR00455; HTHTETR.  
 KW DNA-binding; Hypothetical protein; Transcription regulation.  
 SQ SEQUENCE 228 AA; 24140 MW; A928DE14F404859B CRC64;

Query Match  
 Best Local Similarity 9.0%; Score 7; DB 2; Length 228;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARP 70  
 DB 23 RRRARP 29

RESULT 10  
 ID 09T3Y9 PRELIMINARY; PRT; 245 AA.  
 AC 09T3Y9;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)

Query	Match Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Best local	100.0%	100.0%	18	245	0	0	0
Matches	7	Conservative	0	Mismatches	0	Indels	Gaps
OY	18	TGTTTATL	24				
Db	204	TGTTTATL	210				

DT 01-JUN-2001 (TREMblrel, 17, Created)  
DT 01-JUN-2001 (TREMblrel, 17, Last sequence update)  
DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)  
DE HYPOTHEtical 34.7 KDa PROTEIN (AT3G086500.F17014\_7).  
EN F17014\_7.

RP SEQUENCE FROM N.A.  
RC STRAIN=CV, COLUMBIA;  
RX MEDLINE=21016720; PubMed=11130713;

RA Salinoubat M., Lemcke K., Rieger M., Ansoerg M., Unseld M.,  
RA Fiermann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,  
RA Delany M., Boutry M., Grivell L.A., Mache R., Pulgomech P.,  
RA De Simone V., Choisine N., Artiguenave F., Robert C., Brotler P.,

RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wincker P., Cettolico L., Weissensbach J., Saurin W., Queller F.,  
RA Wurmback E., Drzonek H., Erle H., Jordan N., Bangert S.,  
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.

RA Vezzi A., D'Angelo M., Pallavicini A., Ioppo S., Simonetti B.,  
RA Contrà A., Horstschke K., Kauer G., Loehnert T.-H., Nordstok G.,  
RA Reichelt J., Schafie M., Schoen O., Bargues M., Terol J., Clement J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,  
RA Gordo P., Faudon M., Ponsard-Janus C., Puelletier D., Veruut D.

RA COOKE R., LAURET M., DELGAT L., LAURET C., FUMELLE B., MASSY D.,  
RA DE HAAN M., MAIRE A.C., ALCAZAR J.-P., COTTEAU A., CASACUBERTA E.,  
RA MONFORT A., ARGITOU A., FLORES M., LIGUORI R., VITALE D.,  
RA MANNHAUG G., HAASE D., SCHOOF H., RÜD S., ZACCARATA P., NEWES H.-W.,  
RA MEYER K.F.X., KAU S., THOM C.D., KOO H.I., TALLON I.J., JENKINS J.

RA Paul G., Miltsch J., Sellers P., Gill J.E., Feldbaum T.V.,  
RA Kreis D., Lin X., Nieman M.C., Salzberg S.L., White O., Venter J.C.,  
RA Cressy T.H., Haas B., Mall R., Wu D., Peterson J., Van Aken S.,  
RA Rooney T., Rizzo M., Walts A., Ultebrock T., Fujii C.Y., Shea T.P.,  
RA Kohnen W., Hahn C., Plemen, Clady, Hoffmeyer, Strahm D., Danneberg U.

RN  
 RP  
 SEQUENCE FROM N.A.  
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.  
 RA Bowser L., Cantliff P., Dale J.M., Goldsmith A.D., Hayshtzaki Y.,  
 RA Izhida J., Jiang P.X., Jones T., Kamlya A., Korlin-Neumann G.,  
 RA Kawai T., Lam B., Lee J., Lin J., Liu S.X., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
 RA Seto M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
 RA Yamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 [2]

RA Ecker J.R. ;  
 RT \*Arabidopsis ORF clones. ;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases  
 RN (3)  
 RP SEQUENCE FROM N.A. Chab D. Watanabe M. C. B.

RA Kawai S., Chen H., Chuek R., Noesima E., Meyers R.C., Danti U.  
RA Bower L.J., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,  
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamaya A.,  
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,  
RA Miyatake M., Narasaka M., Nishino M., Oodaira G., S. Palm C. I.  
RA Watanabe M.

RA. Tang C. C., Tortumli M., Yamada K., Yu G., Yu S., Shinozaki K.,  
RA. Piliam P. K., Quach H. L., Sekural T., Setou M., Seki M., Southwick A.,  
RA. Miliute R., Nishida N., Nguyen T., Onoda C., Oshida T., Oshida T.,  
RA. Davis R. W., Theologos A., Ecker J. R.,  
TT "Arabidopsis cDNA clones."

RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases
DR	EMBL: AC012562; AAC51364.1; -
DR	EMBL: AY056087; AAL06975.1; -
DR	EMBL: AY045687; AAK74036.1; -
DR	EMBL: AY045688; AAK74037.1; -

KM Hypothetical protein.  
SQ SEQUENCE 316 AA; 34732 MW; 5B54FCCF59A5BB5B CRC64

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Query Match          9.0%; Score 7; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 23;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

Oy	22	SALNLPQ	28
Db	146	SALNLPQ	152

RESULT	12
Q99X15	

ID	PRELIMINARY:	PRT;	J8/ AA.
Q99X15:			
01-JUN-2001	(TREMblrel, 17,	Created)	
DT			
01-JUN-2001	(TREMblrel, 17,	Last sequence update)	
BT			
01 JUN 2001	(TREMblrel, 10,	Last sequence update)	

DI SA02002001 (Hemphel, 19, Last annotation update  
DE SA0200200 PROTEIN (HYPOTHETICAL PROTEIN SA0207).  
CN SA0200 OR SA0207.  
OS  
OC Staphylococcus aureus (strain N315), and  
CC Staphylococcus aureus (strain Mu50)

05 *Staphylococcus aureus* (Strain mae01)  
06 Bacteria; Firmicutes; Bacillus/Clostridium group;  
07 Bacillus/Staphylococcus group; Staphylococcus.  
08 NCBI\_TaxID=158879, 158878;  
09 [11]

RP SEQUENCE FROM N.A.  
RC SPECIES-S. aureus (strain N315), and S. aureus (strain Mu50).  
RX MEDLINE-21311952; PubMed-11418146;  
NA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,  
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,  
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,  
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.  
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;  
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*

RT EUREUS";  
 RL Lancer 357:1225-1240(2001).  
 DR EMBL: AP003129; BAB41422.1;  
 DR EMBL: AP003358; BAB56369.1;  
 DR InterPro: IPR000515; BPD\_transp.  
 DR Pfam: PF00528; BPD\_transp. 1.  
 KW Complete proteome: Hypothetical protein.  
 SO SEQUENCE 387 AA; 43077 MW; 08F9FB4BACADCB8 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 16; Length 387;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 LTSALNTL 26  
 |||||  
 DB 27 LTSALNTL 33

RESULT 13  
 O97GC3 PRELIMINARY; PRT; 391 AA.

AC O97GC3;  
 DT 01-OCT-2001 (TREMblrel. 18, Created)  
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)  
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE AICAR TRANSFORMYLASE DOMAIN OF PURH-LIKE PROTEIN.  
 GN CAC2445.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_Taxid=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RA MEDLINE-21359325; PubMed-11466286;  
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R.L., Lee H.M., Dupuis J., Qiu D., Hilti J., Wolf Y.I.,  
 RA Tatusov R.L., Sabate F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum";  
 RL J. Bacteriol. 183:4823-4836(2001).  
 DR EMBL: AE007744; AAK80399.1;  
 DR InterPro: IPR002695; AICARFT\_IPMChas.  
 DR Pfam: PF01808; AICARFT\_IPMChas; 1.  
 DR ProDom: PD004666; AICARFT\_IPMChas; 1.  
 KW Complete proteome.  
 SO SEQUENCE 391 AA; 43547 MW; 18642C6BA97E909E CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 16; Length 391;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23  
 |||||  
 DB 58 ATGLTSA 64

RESULT 14  
 O9AX94 PRELIMINARY; PRT; 392 AA.  
 AC O9AX94;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE P0501G01.23 PROTEIN.  
 GN P0501G01.23.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Euphorbiaceae; Oryzae; Oryza.

OX NCBI\_Taxid=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV, NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
 RT clone:P0501G01."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP002819; BAB21094.1;  
 SO SEQUENCE 392 AA; 40501 MW; BB4F44827A7EDC34 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 10; Length 392;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARP 70  
 |||||  
 DB 133 RRRARP 139

RESULT 15  
 O9PSS8 PRELIMINARY; PRT; 490 AA.

AC O9PSS8;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE PUTATIVE WALL-ASSOCIATED KINASE 2.  
 GN H0212B02.2.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Euphorbiaceae; Oryzae; Oryza.  
 OX NCBI\_Taxid=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Han B., Zhou B., Feng Q., Huang Y.C., Chen Z.H., Li Y., Zhu J.J.,  
 RA Tang Y.S., Zhao Q., Liu Y.L., Mu J., Yu Z., Fan D.L., Chen L.,  
 RA Wang Q.J., Zhang L., Lu Y.O., Yu S.L., Zhu J., Liu X.H., Hu X.,  
 RA Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,  
 RA Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.;  
 RT "Oryza sativa Indica (Guanglu14) genomic DNA, chromosome4, BAC  
 RT clone:H0212B02."  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL442007; CAC09346.1;  
 KW Kinase.  
 SO SEQUENCE 490 AA; 52039 MW; 2F1301B08BAZ6EPE CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 10; Length 490;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARP 70  
 |||||  
 DB 345 RRRARP 351

Search completed: June 21, 2002, 08:24:57  
 Job time: 282 sec

